

Errors Corrected by the STIC Systems Branch

Serial Number: 08/487,032 A

CRF Processing Date: 3/24/99
 Edited by: [Signature]
 Verified by: [Signature] (STIC Staff)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/487,032ADATE: 03/25/97
TIME: 10:10:00

INPUT SET: S16452.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: DOUGLAS SMITH
6
7 (ii) TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
8 RELATING TO HELICOBACTER PYLORI FOR
9 DIAGNOSTICS AND THERAPEUTICS
10
11 (iii) NUMBER OF SEQUENCES: 880
12
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: LAHIVE & COCKFIELD
15 (B) STREET: 60 State Street
16 (C) CITY: Boston
17 (D) STATE: Massachusetts
18 (E) COUNTRY: USA
19 (F) ZIP: 02109-1875
20
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
26
27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER: US 08/487,032
29 (B) FILING DATE: 07-JUNE-1995
30
31 (viii) ATTORNEY/AGENT INFORMATION:
32 (A) NAME: Mandragouras, Amy E.
33 (B) REGISTRATION NUMBER: 36,207
34 (C) REFERENCE/DOCKET NUMBER: GTN-001
35
36 (ix) TELECOMMUNICATION INFORMATION:
37 (A) TELEPHONE: (617)227-7400
38 (B) TELEFAX: (617)227-5941
39
40
41 (2) INFORMATION FOR SEQ ID NO:1:
42
43 (i) SEQUENCE CHARACTERISTICS:
44 (A) LENGTH: 1527 base pairs
45 (B) TYPE: nucleic acid
46 (C) STRANDEDNESS: double

RAW SEQUENCE LISTING
PATENT APPLICATION #US/08/487,032A

DATE: 03/25/97

TIME: 10:10:04

INPUT SET: S16452.raw

47 (D) TOPOLOGY: circular
48
49 (ii) MOLECULE TYPE: DNA (genomic)
50
51 (iii) HYPOTHETICAL: NO
52
53 (iv) ANTI-SENSE: NO
54
55 (vi) ORIGINAL SOURCE:
56 (A) ORGANISM: Helicobacter pylori
57
58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
59
60 ATGTGTTCTC AGGAAATTTT ATCAAGCTTG CAAACCATTA TTGCCGAACA ATTTTCTATA 60
61
62 AATATCATCA CTCAGCTTGC TAATAAACTC ACACAAGTTA AAAATCTAAA TTTTTTTGAG 120
63
64 AATAAGACC ATACTATCAA GCTTAACACT ATCCATAACG GACTGCACAT CCGCCCCCTA 180
65
66 AATTATGTCA GTAATCTTTT TTTCAATCTA CAACGCATTA TAGGGCTTAT CAGTCTGTTT 240
67
68 GGGATATTAT TTTCCATTAG TATTTATCTA CCCTTTATAA TGATTTTTGC AACAGTGCCT 300
69
70 TGTATTCTCA TTTCCAACCA TATAGCAAAA AACATAGTG CTTCCATAGA TAAACTTCAA 360
71
72 GACCAAAAAG AAAGCATGCA AAATTACTTA TACTCTGGAC TAGATAACCA AAAGAACAAG 420
73
74 GACAACCTAT TATTAACTT CATGCTAAAT TTTCAACATA AATTATTTGA AACAAAAGAA 480
75
76 TTGTATCTCA ATAATTTTGT GAAAGTAGCC CAAAAAACT TAATATTTAC CATATATGCT 540
77
78 GATGTTTTAA TCACCACTCT AAGTATTGCA CTATTTTTTC TAATGGTTTT TATTATCCTT 600
79
80 TCAAAATTA TGGTGTGGG AGCAATTGCT GGGTATATCC AAGCATTTAG CTCTACCCAA 660
81
82 CAACAACCTAC AAGATTTATC ATTTTATGGA AAGTGGTTTT TTGCTATCAA TAAATACTTT 720
83
84 GAAAATTATT TCTGTATTTT AGATTACAAA ATACCGAAAC CAGAAACACA AATCAAATTA 780
85
86 GAAGAAAAAA TCCATAGCAT TACATTTGAA AATATTAGTT TCTCTTATCC TAATTCAAAA 840
87
88 CTTATTTTTG AAAACTTTAA TCTCTCTTA CACTCTAATA AAATTTATGC ATTAGTCGGC 900
89
90 AAGAATGCTA GCGGAAAAAG CACGCTGATT AATTTATTAT TAGGTTTTTA TACCCCAAAT 960
91
92 TCAGGTCAAA TTATCATTA TAACAAATAC CCATTACAAG ACTTGGAAC AAATAGCTAC 1020
93
94 CATCAACAAA TGAGTGCCAT ATTTCAAGAT TTTTCTCTTT ATGCTGGGTA TAGCATTGAT 1080
95
96 GATAATCTTT TTATGCAAAA CAATATCACT AAAGAGCAAT TGAAGCAAAA AAGAGAAATA 1140
97
98 CTAAATCTT TTGATGAGAA TTTTCAAAAT TGTCTTAATG ATTGCAACAA CACACTATTT 1200
99

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/487,032ADATE: 03/25/97
TIME: 10:10:08

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100 GGAGCGCAAT ATAATGGGGT AGATTTTCT TTAGGTCAA AGCAACGCAT AGCTACCATG 1260
101
102 AGAGCCTTTT TAAAACCAAG TAATTGCATT GTTTTAGATG AGCCAAGCAG CGCCATCGAT 1320
103
104 CCCATTATGG AAAAAGAGTT TTTAGATTTT ATTTTAAAA AATCGCAATC TAAGATGGCT 1380
105
106 TTAATTATTA CACACCGCAT GAATAGTGTC AAGCAAGCTA ATGAAATTAT CGTGTTAGAT 1440
107
108 CAAGGCAAAC TAATAGAACA GGGCAACTTT GAAACCCTTA TGAAAAACA GGGATTATTT 1500
109
110 TGCGAATTGT TTTTGAAACA ACAATAC 1527
111
112

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

132 ATGGAGCGCA AGACGCTCCA GAGCATTTTA TGTTTAATAA AAAAAGAAAT GATGAGACCA 60
133
134 AAAGGTATTC TAATGAATTG TTGCAGGCT TGGAAACACC AGGTTCTTAA GCAAAGCAG 120
135
136 ACAGGTTTAG TGGTGTGAG CATTATCTCT TCTACAGCCC CCTTTATTGG TTTGTTTGGG 180
137
138 ACGGTAGTTG AAATTTTAGA AGCGTTTAAC AATTTGGGCG CGTTAGGTCA AGCTTCTTTT 240
139
140 GGAGTGATCG CACCCATTAT TTCTAAGGCG CTTATCGCCA CCGCTGCAGG GATTTTAGCA 300
141
142 GCCATTCCAG CCTATTCTTT TTACTTGATC TTAAAGCGCA AGGTGTATGA TTTATCGGTT 360
143
144 TATGTGCAGA TGCAAGTGGA TATTTTGTCT TCTAAAAA 399
145
146

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

INPUT SET: S16452.raw

153 (D) TOPOLOGY: circular
154
155 (ii) MOLECULE TYPE: DNA (genomic)
156
157 (iii) HYPOTHETICAL: NO
158
159 (iv) ANTI-SENSE: NO
160
161 (vi) ORIGINAL SOURCE:
162 (A) ORGANISM: Helicobacter pylori
163
164 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
165
166 ATGCATGAAC GCATTGAAAG AGGTATTRGA AATAATGAAT GTAAAGAAAT TTTTGGCAAT 60
167
168 GAACTCAAAC AAAGAAAGAC AAAATTGATT GAAGACATAG AACGGCGGTT CAAAGAATGC 120
169
170 GAGGAACAAT TCCGTGGAAG TGTAGGAAAA AATATTGAAC AACTTGAAGA AAGAGTTAAA 180
171
172 GATTCTCTAG CGATTATAAA ACGCATCAAT AACCTTGGTC TTAATCCTAA TTCTAATTTT 240
173
174 AATATGGATA GCGGCATTGA TACAATAGGC TTATTTAGTT CAATAGGAGG TTTGGTGTTG 300
175
176 CTTCTATTGA CGCCTGTAGT AGGTGAGTTT GCGTTAATTG CAGGAGTGGG TTTAGCATTA 360
177
178 GTGGGGGTAG GTAAATCAAT ATGGAGTTTT TTTGATTGAG ATTATAAAAA ATCCCAACAA 420
179
180 AGAAAAGAAG TGGATAAGAA TTTACATCAA ATTTGCGAAA AATTGTGCAG GATG 474
181
182
183 (2) INFORMATION FOR SEQ ID NO:4:
184
185 (i) SEQUENCE CHARACTERISTICS:
186 (A) LENGTH: 336 base pairs
187 (B) TYPE: nucleic acid
188 (C) STRANDEDNESS: double
189 (D) TOPOLOGY: circular
190
191 (ii) MOLECULE TYPE: DNA (genomic)
192
193 (iii) HYPOTHETICAL: NO
194
195 (iv) ANTI-SENSE: NO
196
197 (vi) ORIGINAL SOURCE:
198 (A) ORGANISM: Helicobacter pylori
199
200 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
201
202 ATGCCTGGCG TGTATCAAAT GAGTATAGAG CCTCTTTTAA AAGAATGCCA AGAATTAGTG 60
203
204 GGTTTAGGCA TAAAAGCCGT TTTATTGTTT GGCATTCCTA AACATAAGGA CGCTACAGGA 120
205

INPUT SET: S16452.raw

206 AGCCATGCGT TAAATAAGGA TCACATTGTC GCAAAAGCTA CGAGAGAAAT TAAAAAACGA 180
207
208 TTTAAGGATT TGATCGTTAT AGCGGATTTG TGTTTTTGCG AATACACCGA CCATGGGCAT 240
209
210 TGCGGGATTT TAGAAAACGC TTCTGTGTCT AACGATAAAA CGCTAAAGAT TTTAAATCTT 300
211
212 CAAGGGCTTA TTTTGCTGAA AGCGGTGTGG ATATTC 336
213
214

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...195

(D) OTHER INFORMATION: /note= "FLAGELLAR HOOK-ASSOCIATED PROTEIN 1

HAP1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

238
239
240 GTGGAAAACA ACAAGAGTTT AAAGCATGCG AATGAGTTAA GGGATAAGCG AGATGAATTA 60
241
242 GAGTTTCATT TGCGAGAGCT TTTCGGGGGG AATGTTTTTA AAAGCAGCAT TAAAACCCAT 120
243
244 TCGCTCACAG ATAAAGACTC AGCGGACTTT GATGAGAGCT ATAACCTTAA TATCGGGCAT 180
245
246 GGGYTCAATA TSATA 195
247
248

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1857 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

DDDDD	CCCCC	SSSSS	22222
DD DDD	CC C	SS SS	22 22
DD DD CC		SSS	22
DD DD CC		SSS	222
DD DD CC		SSS	222
DD DDD	CC C	SS SS	22 22
DDDDD	CCCCC	SSSSS	2222222

DDDDD	CCCCC	SSSSS	22222
DD DDD	CC C	SS SS	22 22
DD DD CC		SSS	22
DD DD CC		SSS	222
DD DD CC		SSS	222
DD DDD	CC C	SS SS	22 22
DDDDD	CCCCC	SSSSS	2222222

Username DCS_2
Machine DCS_2
Comment

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PAGE: 6

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/487,632A

DATE: 03/25/97

TIME: 10:10:36

INPUT SET: S16452.raw

******* PREVIOUSLY ERRORED SEQUENCES - EDITED *******

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DD DD CC		SSS	222
DD DD CC		SSS	222
DD DDD	CC C	SS SS	22 22
DDDDD	CCCCC	SSSSS	2222222

DDDDD	CCCCC	SSSSS	22222
DD DDD	CC C	SS SS	22 22
DD DD CC		SSS	22
DD DD CC		SSS	222
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Machine DCS_2
Comment

Date 97.03.25
Time 10:11:03
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Copies 1
File \spool.net\38._SP

40867 (2) INFORMATION FOR SEQ ID NO:880:

40868

40869

(i) SEQUENCE CHARACTERISTICS:

40870

(A) LENGTH: 363 amino acids

40871

(B) TYPE: amino acid

40872

(D) TOPOLOGY: linear

40873

40874

(ii) MOLECULE TYPE: protein

40875

40876

(iii) HYPOTHETICAL: YES

40877

40878

(vi) ORIGINAL SOURCE:

40879

(A) ORGANISM: Helicobacter pylori

40880

40881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

40882

40883 Met Lys Phe Phe Leu Leu Lys Lys Phe Ser Xaa Phe Leu Asn Thr Gln
40884 1 5 10 15

40885

40886 Thr His Phe Asn Leu Lys Arg Leu Asn Ala Ser Ser Phe Leu Leu Glu
40887 20 25 30

40888

40889 Thr Phe Ser Lys Glu Lys His Ala Phe Val Val Asp Leu Ser Ala Pro
40890 35 40 45

40891

40892 Tyr Ile Gly Leu Ser Lys Lys Pro Pro Glu Ser Val Leu Lys Asn Thr
40893 50 55 60

40894

40895 Leu Ala Leu Asp Phe Cys Leu Asn Lys Phe Thr Lys Asn Ala Lys Ile
40896 65 70 75 80

40897

40898 Leu Gln Ala Asn Val Ile Asp Asn Asp Arg Ile Leu Glu Ile Lys Gly
40899 85 90 95

40900

40901 Ala Lys Asp Leu Ala Tyr Lys Ser Glu Thr Phe Ile Leu Arg Leu Glu
40902 100 105 110

40903

40904 Met Ile Pro Lys Lys Ala Asn Leu Met Ile Leu Asp Gln Glu Lys Cys
40905 115 120 125

40906

40907 Val Ile Glu Ala Phe Arg Phe Asn Asp Arg Val Ala Lys Asn Asp Ile
40908 130 135 140

40909

40910 Leu Gly Ala Leu Pro Pro Asn Ile Tyr Glu His Gln Glu Glu Asp Leu
40911 145 150 155 160

40912

40913 Asp Phe Lys Gly Leu Leu Asp Ile Leu Glu Lys Asp Phe Leu Ser Tyr

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/487,032ADATE: 03/25/97
TIME: 10:11:04

INPUT SET: S16452.raw

40914		165		170		175
40915						
40916	Gln His Lys Glu Leu Glu His Lys Lys Asn Gln Ile Ile Lys Arg Leu					
40917		180		185		190
40918						
40919	Asn Ala Gln Lys Glu Arg Leu Lys Glu Lys Leu Glu Lys Leu Glu Asp					
40920		195		200		205
40921						
40922	Pro Lys Thr Leu Gln Leu Glu Ala Lys Glu Leu Gln Thr Gln Ala Ser					
40923		210		215		220
40924						
40925	Leu Leu Leu Thr Tyr Gln His Leu Ile Asn Arg Arg Glu Asn Arg Val					
40926		225		230		235
40927						240
40928	Ile Leu Lys Asp Phe Glu Asp Lys Glu Cys Met Ile Glu Ile Asp Lys					
40929		245		250		255
40930						
40931	Ser Met Pro Leu Asn Ala Phe Ile Asn Lys Lys Phe Thr Leu Ser Lys					
40932		260		265		270
40933						
40934	Lys Lys Lys Gln Lys Ser Gln Phe Leu Tyr Leu Glu Glu Glu Asn Leu					
40935		275		280		285
40936						
40937	Lys Glu Lys Ile Ala Phe Lys Glu Asn Gln Ile Asn Tyr Val Arg Asp					
40938		290		295		300
40939						
40940	Ala Ala Glu Glu Ser Val Leu Glu Met Phe Met Pro Val Lys Asn Ser					
40941		305		310		315
40942						320
40943	Lys Ile Lys Arg Pro Met Asn Gly Tyr Glu Val Leu Tyr Tyr Lys Asp					
40944		325		330		335
40945						
40946	Xaa Lys Xaa Gly Leu Gly Lys Thr Lys Lys Arg Ile Ser Ser Phe Tyr					
40947		340		345		350
40948						
40949	Lys Thr Gln Xaa Arg Met Ile Xaa Gly Cys Xaa					
40950		355		360		
40951						
40952						
40953						
40954						

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/487,032A

DATE: 03/25/97

TIME: 10:11:07

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Line

Error

Original Text